

# **EXHIBIT B**

# Alignment of nucleotide sequences of glutamine synthetase genes

		1		50
2247	(1)	-----GTGGCGTTTGAA-ACCCCGGAAGAAATTGTCAAGTT		
13032	(1)	-----GTGGCGTTTGAA-ACCCCGGAAGAAATTGTCAAGTT		
CEfInA1	(1)	-----GTGGCGTTTAAAC-ACCCCGGAAGAGTAACCAAGTT		
CEfInA2	(1)	-----GTGGCCTCGAGCCCGACAACCAACCCGGATGAGATCCTCAAGTT		
MtugInA2	(1)	-----ATGACCGACAGAGGAATTCTTCTTCG		
MtugInA3	(1)	-----ATGACAGCCACACCGCTTCCGCGGCCGCGAT		
MtugInA4	(1)	GTGACCGGCCCGGTTCGCCGCCGTTGGCGTGACCGAGTTGAGCGACT		
MtugInA1	(1)	-----GTGACCGAAAG-ACGCCCGACGACGTTCTCAAACT		
Consensus	(1)	GTGGCGGATGA ACCCCGGA GAA T GTCAAGTT		
		51		100
2247	(36)	CATCA AGGATGAA AACGTGAGTTCGTTGACGTTGATTACCCG		
13032	(36)	CATCA AGGATGAA AACGTGAGTTCGTTGACGTTGATTACCCG		
CEfInA1	(36)	CATCA AGGATGAA AACGTGAGTTCGTTGACGTTGATTACCCG		
CEfInA2	(45)	CATCC GGGACAAT GACATCAACTGGGTGACGTTCCAGTTACCCG		
MtugInA2	(30)	TACCC TGGAGAGACGCGACATCCGCTTCGTCGGCTGTGGTTACAG		
MtugInA3	(33)	CGCCCAATTGGAGGCAGAGGCGGTGACACCGTCATCGCACCGTCTGTA		
MtugInA4	(51)	GGTCG CCGCCGGT GACGTGACACCGTCATCGTCGGTTACCCG		
MtugInA1	(36)	TGCGA AGGACGAG AAGGTGGAATATGTGACGTTCCGGTTCTGTG		
Consensus	(51)	CATCA AGGA GAA GACGTGACGTTCTGACGTTCCGGTTACCCG		
		101		150
2247	(80)	ACCTTCCGGGACCGAGCAGCACTTCAGCATCCGAGGTGCCAGCTTCGAT		
13032	(80)	ACCTTCCGGGACCGAGCAGCACTTCAGCATCCGAGGTGCCAGCTTCGAT		
CEfInA1	(80)	ACCTTCCGGGACCGAGCAGCACTTCAGCATCCGAGGTGCCAGCTTCGAT		
CEfInA2	(89)	ACGTTCCGGGACCGAACAGCAGCTGTCCGTGCCCGCCGCGCATTCGAC		
MtugInA2	(77)	ACGTGCTCGGTTTCTCAAGTCGGTGGCATGCCCCAGCCGAACGGA		
MtugInA3	(83)	ACCCCGCGGACTACCCAGCGCAAGACGTTGCCGATACGCCGACGAA		
MtugInA4	(95)	ACATGCAAGGC CCGGTGGCCGGCAACGGAATTCGGGCGGCA		
MtugInA1	(80)	ACCTGCTTGGCATCATGCAGCACTTCAGATTCGGGCTTGGGCTTTGAC		
Consensus	(101)	ACCTTCCGGGACCGAGCAGCACTTCAGCATCCG GACGCCGGCTTCGA		
		151		200
2247	(130)	GCAGATACAGTCGAAGAAGGTCTCGCATTCGACGGATCCTCGATCCGTGG		
13032	(130)	GCAGATACAAATCGAAGAAGGTCTCGCATTCGACGGATCCTCGATCCGTGG		
CEfInA1	(130)	GAGGACGCCATCGAGGAGGGCCTCGCCTTCGACGGTTCCTCCATCCGTGG		
CEfInA2	(139)	GAATCGGCCATGGAAAACGGACTGCCCTTCGACGGGTATCGATCAGCGG		
MtugInA2	(126)	GGGCGCTTCGAGGAAGGCATCGGCTTCGACGGATCCTCGATCGAGGG		
MtugInA3	(132)	CAGATTCGCCAA TCCTGCCCTCGGCCAGTCCGCTGTGGCA		
MtugInA4	(138)	T TCGTCGACGACATAGCCACCGCGGCGTGGAGTGGTGCAG		
MtugInA1	(130)	AAGAGCGTGTGTGACGACGGCTTGGCCTTTCGACGGCTCTCGATTCGCGG		
Consensus	(151)	G G CGC TTGGA GA GGCCTCGCCTTCGACGG TCCTCGATCCG GG		
		201		250
2247	(180)	CTTCACCACGATCGACGAATCTGACATGAATCTCCTGCCAGACCTC GGA		
13032	(180)	CTTCACCACGATCGACGAATCTGACATGAATCTCCTGCCAGACCTC GGA		
CEfInA1	(180)	TTTCACCACCATTGATGAATCCGACATGAACCTGCTGCCGGATCTG GCC		
CEfInA2	(189)	ATACACCACTGTGACGATTCGACATGATGCTGCTGCCGGATCTG TCC		
MtugInA2	(174)	CTTGGCGGGTCTCGGAATCCGATACGGTGGCGACCGGGACC		
MtugInA3	(174)	TACGTTTGTATCGACCAATCCAGTATTCATTCACCGACAGATCAATG		
MtugInA4	(180)	TTATCTGCTGGCGGTGACGTGACCTGAAACACGTTGCCCGGCTAT CGG		
MtugInA1	(180)	GTTCAGTCCATCCACGAATCCGACATGTTGCTCTTCCCGATCCC GAG		
Consensus	(201)	TTACACCACGATCGACGAATCCGACATGAA CTGCTGCC GACCTC G		
		251		300

2247	(229)	ACGGCCACCCCTTGATCC	ATTCCGCAA	GGCAAGACCCTGAACGT
13032	(229)	ACGGCCACCCCTTGATCC	ATTCCGCAA	GGCAAGACCCTGAACGT
CEFlnA1	(229)	ACGGGAAGATCGATCC	GTTCCGCAA	GGCAAGACCCTGAACAT
CEFlnA2	(238)	ACGGGTTTCATCGACCC	GTTCCGCA	GTCGAAGACCTCAACAT
MtuglnA2	(218)	CGTCGACCTTCAGGT	GCTGCCCTG	GGCCA
MtuglnA3	(224)	TGGTCGGCGATCAACGT	CTCCGCAT	CGA
MtuglnA4	(229)	ATGGCCAGTTGGGACACCG	CTACGGCGATAT	GTTGATGACCCCGGACTT
MtuglnA1	(229)	ACGGCCCGCATCGACCC	GTTCCGCGC	GGCCAAGACCTGAATAT
Consensus	(251)	ACGGCGACCATCGACCC	GTTCCGCA	GGCAAGACCCTGAAC T
		301		350
2247	(273)	TAAGTTCTTCGTTACGATCC	TTACCCCGC	GAGGCATTCTCCCGCGAC
13032	(273)	TAAGTTCTTCGTTACGATCC	TTACCCCGC	GAGGCATTCTCCCGCGAC
CEFlnA1	(273)	CAAGTTCTTCGTTCCAT	GACCCCTTCACCCGT	GAGGCATTCTCCCGCGAC
CEFlnA2	(282)	CAAGTTCTTCGTTCCAT	GACCCCTATACCCGGGAAC	ATTCTCCCGGAT
MtuglnA2	(250)	AGTTC	CGGCCACCACT	CAGCGCGGATGTTTGCAGATCA
MtuglnA3	(254)	GTCCGCTTTCGGCAT	CATGGCGACGGGT	TGGCGTG
MtuglnA4	(279)	GTCACCTCTGGGGTGATT	CCTTGGCTACCCGGGAAC	CGCGGTGGTATCG
MtuglnA1	(273)	CAACTTCTTGTGCACGACCC	CTTACCCCTGGAGCGT	ACTCCCGCGAC
Consensus	(301)	TAAGTTCTTCGTTCCACGACCCCTT	CACCCGGGAGGCGT	TCTCCCGCGAC
		351		400
2247	(322)	CCACGCAACGTAGCA	CGCAAGGCAGAGCAGT	ACCTGGC
13032	(322)	CCACGCAACGTGGCA	CGCAAGGCAGAGCAGT	ACCTGGC
CEFlnA1	(322)	CCCGCAATGTGGCA	CGTAAGGCAGAGCAGT	CTCTGGC
CEFlnA2	(331)	CCCGCAACATCGCC	CGCAAGGCAGAGCAGT	ACCTGGC
MtuglnA2	(293)	CCATGCGGACGGCTCGCC	GTCTGGCGCGACCCG	CGGCACGTG
MtuglnA3	(299)	CGGGTTCTTCGAGCAGG	ACGGACACCGGT	CTGCAGCCG
MtuglnA4	(329)	CGGACGTGGTCTGGGCG	ACGGCAGCGAGGT	CGCCGTCTCG
MtuglnA1	(322)	CGCGCAACATCGCC	CGCAAGGCAGAGC	ACTACCTGAT
Consensus	(351)	CC CGCAAC TGGC	CGCAAGGCAGAGCAGT	ACCTGGC CTGCACCGG
		401		450
2247	(369)	CATTGCAGACACCTGCAACT	TGGCGCCGAGGCT	GAGTCTACCTCTTCG
13032	(369)	CATTGCAGACACCTGCAACT	TGGCGCCGAGGCT	GAGTCTACCTCTTCG
CEFlnA1	(369)	CATCGCCGACACCTGCAACT	TGGCGCCGAGGCT	GAGTCTATCTCTTCG
CEFlnA2	(378)	TTTGGCCGACAGCTGTA	ACTTGGCGCCGAA	GCCGAGTCTACATCTTCG
MtuglnA2	(337)	TTGGCGCGGAGGTC	ACGAAGGC	G
MtuglnA3	(345)	AGGAACACTGACCGGAT	GAGCGCGGCTT	GCTGATCGCGCATCGACG
MtuglnA4	(379)	ATTCTGCGCGTCAAGT	CGATCGGCT	CAAGGC
MtuglnA1	(369)	CATCGCCGACACCGCAT	ACTTGGCGCCGAGGCT	GAGTCTACATTTTCG
Consensus	(401)	CATCGCCGACACCTGCAACT	TGGCGCCGAGGCT	GAGTCTACCTCTTCG
		451		500
2247	(419)	ACTCCGTTTCGCTACT	CCACCGAGAT	GAACTCCGGCTTCTACGAAGTAGAT
13032	(419)	ACTCCGTTTCGCTACT	CCACCGAGAT	GAACTCCGGCTTCTACGAAGTAGAT
CEFlnA1	(419)	ACTCCGTTTCGCTACT	CCACCGACATCAACT	CCGGTTCTACCATGTGGAC
CEFlnA2	(428)	ACTCCGTTTCGCTACT	CCAGTCCCAAT	GCGGCAATCCACGAGGTGGAT
MtuglnA2	(380)	GCTACGTGCATCCGAAAT	CGAG	TTCTTCTGCTCAAG
MtuglnA3	(395)	CGGTAAATCGCCACGAAGT	CGAA	TTCTCTTGGTTCGAC
MtuglnA4	(425)	CCGATGTGGCCACCGAGCT	GAGTTCATCGT	G
MtuglnA1	(419)	ATTCTGTGAGCTT	CGACTCGCGCC	CAACGGCTCTTCTACGAGGTGGAC
Consensus	(451)	ACTCCGTGCGCTACGACACCGAG	TCAAC CCG	TTCTACGAGGTGGAT
		501		550
2247	(469)	ACCGAAGAAAGGCTGGT	GGAACCGTGGC	AAAGGAACCAACCTCGACGGAAC

13032	(469)	A CCGAAGAGGGGTGGTGGAAACCGTGGCAAGGAACCAACCTCGACGGCAG
CEfInA1	(469)	ACCAACGAGGGTTGGTGGAAACCGTGGCGTGAGACCAACCTCGATGGCAG
CEfInA2	(478)	TCCGTGGAGGGGTGGTGGAAACAGTGGTTCCCGGGAGAACCGGACGGCAG
MtugInA2	(418)	CCC-----GGACCGGAGGACGG-----TCGGTGGCGG
MtugInA3	(433)	GGGGA-----C-----G-GCCAGCGGTGCCT-----TCGAGC-CTG
MtugInA4	(472)	CGCC-AGGCA-TGGGCGAGCGG-GTA-----TCGCGGGGTG
MtugInA1	(469)	GCCATCTCGGGGTGGTGGAAACACGGCGCGCGACCGAGGCAGGCGACGGCAG
Consensus	(501)	CCGA GAGGGCTGGTGGAAACCGTGGC GGA ACCAACCTCGACGGCAG
		551 600
2247	(519)	CCCAAAACCTGGGCGCAAAGAACCGGTCAAGGGTGGGTACTTCCAGTAG
13032	(519)	CCCAAAACCTGGGCGCAAAGAACCGGTCAAGGGTGGGTACTTCCAGTAG
CEfInA1	(519)	CCCCAACACCGGTTCCAAGAACCGCTCAAGGGCGGTACTTCCCGCTCG
CEfInA2	(528)	CAGGAACCTGGGTACAAGGTACGGCAGAGGGTGGTACTTCCCGGTGG
MtugInA2	(446)	TCCC-----GGTGG-A-----CAACGCGGCTATTTCGACCAAG
MtugInA3	(463)	T-----GGGC-C-----AGTACGG-TGTGGCGGGG
MtugInA4	(505)	ACCC-C-GGGC-AGCGA-CTACAACATCGACTACGCGATATTGG
MtugInA1	(519)	TCCCAACCGGGGTACAAGGTCCGCCACAAGGGCGGGTATTTCGAGTGG
Consensus	(551)	CCCCAACC GGGCC AAG CCGC CAAGGGCGGCTACTTCCAGTGG
		601 650
2247	(569)	CA CCATACGACCAAACCGTTGACGTGCGCGATGACATGGTTCGCAACC
13032	(569)	CA CCATACGACCAAACCGTTGACGTGCGCGATGACATGGTTCGCAACC
CEfInA1	(569)	CA CCCTACGACCAAGACCGTGGACGTCCGCGATGACATGGTCCGCAACC
CEfInA2	(578)	CA CCCTATGACCACTTCAGGACCTGCGCGACACCATTCGTGAGACCC
MtugInA2	(479)	CG-GTGCACGACTCCGCCTTGAAGTTTCGCGCCACGCGATCGATGCCG
MtugInA3	(488)	TG-CTCGAGCAGGAGGCGTTTG-TCGCGGATGTCAACCCGCGGCAA
MtugInA4	(545)	CATCCTCGCGGATGGAGCCGTTG-CTGCGGACATCCGGTTGGGTAA
MtugInA1	(569)	CC-CCCAACGACCAATAAGTCGACCTGCGCGACAAGATGCTGACCAACC
Consensus	(601)	CA CCCTACGACCAA CCGT GAC TCGCGGATGACATGGT GCGAACC
		651 700
2247	(617)	TGCGAGCTTCGGGCTTCGGTCTTGAGCGTTTCACCACGGAAGTCGG-T
13032	(617)	TGCGAGCTTCGGGCTTCGGTCTTGAGCGTTTCACCACGGAAGTCGG-T
CEfInA1	(617)	TGCGTACGCGGGTTTCACCTGGAGCGTTTCACGACGAGGTCGG-T
CEfInA2	(626)	TGGCGGAGATCGGGTTCAACGTGGAGCGTTCCACCATGAGATGGGCAGT
MtugInA2	(527)	TGGAATTGATGGGCACTCTGGTGGAGTTCAGCCATCAGGAAGGGC-A
MtugInA3	(533)	CGGCAG-CAGGCAATCGGTATCGAGCAGTTCATCCGGAATACGG-T
MtugInA4	(590)	TGGCGGTGCGGGTCTGCGATTGAGGCGGTTCAAGCGGAATGCAA-C
MtugInA1	(617)	TGATCAACTCGGGCTTCATCTGGAGAAGGGCGACCAAGAGTGGGCAGC
Consensus	(651)	TGGCAG CCGGCTTC C CTGGAGCGTTTCACCACGGAAGTCGG T
		701 750
2247	(664)	GGCGGACAGCAGGAATCAACTACCGCTTCAACACCATGCTCCAGGCGGC
13032	(664)	GGCGGACAGCAGGAATCAACTACCGCTTCAACACCATGCTCCAGGCGGC
CEfInA1	(664)	GGCGGACAGCAGGAGATCAACTACCGCTTCAACACCGCTCTGCAGGAGC
CEfInA2	(676)	GGTGGTCAGCAGGAGATCAACTACCGTTCAACACCGCTGCTCGCGGAGC
MtugInA2	(574)	CCCGGCCAGCAGGAGATCACTCGGGTTTGGCGAGGCTCTGTGATGGC
MtugInA3	(577)	GCAACCAATTCGAGATCTGTTAGCGCCGACGCGCGGTCGCGGCCGC
MtugInA4	(637)	ATGGGCCAGCAGGAGATCGGGTTTGGTTACGACGAGGCGCTGGTCACTG
MtugInA1	(667)	GGCGGACAGCGCGAGATCAACTACCGTTCAATTGCTGCTGCAGCGCGC
Consensus	(701)	GGCGGCCAGCAGGAGATCAACTACCG TTCAACACCGTCTGCACGC GC
		751 800
2247	(714)	AGATGATATCCAGACCTTCAAGTACATCATCAAGAACACCGCTCGGCTCG
13032	(714)	AGATGATATCCAGACCTTCAAGTACATCATCAAGAACACCGCTCGGCTCG

CEFl nA1	(714)	CGATGACATT CAGACCTTCAAGTACATCGTGAAGAACACCGGAGCCCTGC
CEFl nA2	(726)	CGATGACCTCCAGACCTTCAAGTACGTGGTGAAGAACACCGGGAAGGCCG
Mtugl nA2	(624)	TGACAACGTGATGACCTTCCGTACGTATCAAGAAGTCGGCTGGAAG
Mtugl nA3	(627)	CGATCAGCTGGTCTGACCCGCTCATCATCGGCCGTACCGCCGGCCGGC
Mtugl nA4	(687)	CGACAACCATGCCATCTACAAGAAGGGGCCAAGGAATCGCCGACGAGC
Mtugl nA1	(717)	CGACGACATGCAGTTGTACAAGTACATCATCAAGAACACCGCTGGCAGA
Consensus	(751)	CGATGACAT CAGACCTTCAAGTACATCATCAAGAACACCGC CGCC GC
		801 850
2247	(764)	ACGGCAAGGCTGCAACCTTCATGCCTAAGCCACTGGCTGGCGACAACGGT
13032	(764)	ACGGCAAGGCTGCAACCTTCATGCCTAAGCCACTGGCTGGCGACAACGGT
CEFl nA1	(764)	ACGGCAAGGCTGCCACCTTCATGCCCAAGCCGCTGGCCGGTGACAACGGC
CEFl nA2	(776)	TCCGTAAATCCGCCACCTTCATGCCCAAGCCGCTGGCTGATGACGCCGT
Mtugl nA2	(674)	AGGGCGCCCGGGCGTCTTCATGCCCAAGCCATTCCGCCAGCACCCGGC
Mtugl nA3	(677)	ACGGGTTACGCGTGAGCTATCGCCAGCGCCCTTCGCCGAAGTATCGGA
Mtugl nA4	(737)	ACGGCAAGAGCCTAACGTTTCATGCGGAAATACGATGAACGGGAAGGT
Mtugl nA1	(767)	ACGGCAAAACGGTCAAGTTTCATGCCCAAGCCGCTGTTCCGCCACAACGGG
Consensus	(801)	ACGGCAAG C GC ACCTTCATGCCCAAGCCACTGGCTGG GACAACGGT
		851 900
2247	(814)	TCCGGCATGCACGCTCACCAGTCCTCTGGAAGGACGGCAAGCCACT
13032	(814)	TCCGGCATGCACGCTCACCAGTCCTCTGGAAGGACGGCAAGCCACT
CEFl nA1	(814)	TCCGGCATGCACGCCACCAGTCCTCTGGAAGGACGGCAAGCCACT
CEFl nA2	(826)	TCCGGCATGCACATCCACCAGTCGCTGTGGAAGGACGGCAAGCCCT
Mtugl nA2	(724)	TCCGCCATGCACACCCACATGAGCCTGTTCCAGGGTGATGTCAACCGGTT
Mtugl nA3	(727)	TCCGGTCCCAGCAACACCTCTCGCTGACTATGTCGGAAGCGATGCT
Mtugl nA4	(784)	AATAGCTGTGACATCCATGTCTCGCTCGGTGGCACGGATGGCTCCCGGT
Mtugl nA1	(817)	TCCGGCATGCACGTGTCAACAGTCGCTGTGGAAGGACGGGGCCCGCT
Consensus	(851)	TCCGGCATGCAC CCCACCAGTCGCTGTGGAAGGACGGCAAGCCGCT
		901 950
2247	(861)	CTTCCACGATGACTCCGGCTACGCCAGGCGTGTCCGACATCGCCGCTAC
13032	(861)	CTTCCACGATGACTCCGGCTACGCCAGGCGTGTCCGACATCGCCGCTAC
CEFl nA1	(861)	CTTCCACGACGACTCCGGCTACGCCAGGCGTGTCCGACATCGCCGCTAC
CEFl nA2	(873)	CTTCCATGATGAAGCCGGTTATGCCAACCTGTCCGAGATGGCCGCTAC
Mtugl nA2	(774)	CCACAGCGCTGATGATCCGCTGCAGCTGTGTCGGGAAGTGGTAAATCG
Mtugl nA3	(774)	GTTCTCCGGTGGGAGCTGGAGCAGCTGGCATGACCTCGGCCGGGAGGC
Mtugl nA4	(834)	GTTTGCCGACAGTAAGGGCCGCAAGGCATGTCGTCGATGTTCCGACG
Mtugl nA1	(864)	GATGTACGACGAAGACGGTTATGCCGGTCTGTCCGACACGGCCGTCAT
Consensus	(901)	CTTCCACGATGA GACCGGCTACGC GGCCTGTCCGACATGGCCG TAC
		951 1000
2247	(910)	TACATCGGCGGCATCCTGCACCACGCAAGGCGTGTCTGGCGTTACCA
13032	(910)	TACATCGGCGGCATCCTGCACCACGCAAGGCGTGTCTGGCGTTACCA
CEFl nA1	(910)	TACATCGGTGGCATCCTGCACCACGCGGTCGGTCTGGCGTTACCA
CEFl nA2	(922)	TATGTCCGTGGTCTGCTCAAGCATGCCCGCGGTCTGGCTTTACCA
Mtugl nA2	(820)	TTTCATCGCCGGGATCCTGGAGCAGGTTGGAGATCAGCGCGGTACAA
Mtugl nA3	(823)	GCGGTGGCAGGAGTGCCTC-GGGATACCGGACGCCAAGGCATCCTGT
Mtugl nA4	(883)	TTCTGCGCCGGCCAGTTGG-CCAGTTTCGCGAATTCACGCTGTGCTATG
Mtugl nA1	(913)	TACATCGGCGGCCTGTTACACCACGCGCCGTGGCTCTGGCGTTACCA
Consensus	(951)	TACATCGGCGGCATGCTGCACCACGC GGCCTGTCCGACATGGCCG TACCA
		1001 1050
2247	(959)	ACGCAACCCCTGAACTCCTACCACCGTCTGGTTCCAGGCTTCGAGGCTCCA
13032	(959)	ACGCAACCCCTGAACTCCTACCACCGTCTGGTTCCAGGCTTCGAGGCTCCA
CEFl nA1	(959)	ACCCGACGCTGAACTCCTACCATCGCTGGTTCCCGGGCTTCGAGGGCCCC



CEFlnA2	(971)	ACCGGACCCCTGAATTCCTACAACCGTCTGGTGGCCGGTTTCGAGGGCCCG
MtugInA2	(869)	ATCAGTGGGTCAACTCTTACAAGCGGCTGGTGCAGGGCGGCGAAAGCGCC
MtugInA3	(872)	GCGGATCGATCGTGTCCGGTCTCGGAATCCGACCCGGTAACTGGGCGGGA
MtugInA4	(932)	CGCCGACCATTAAGTCCTACAAGCGATTTCGGATAGCAGTTTCGGCCCG
MtugInA1	(962)	ACCGGACGGTGAAGTCCTACAAGCGGCTGGTTCGGGTTCGAGGGCCCG
Consensus	(1001)	ACCGGACCCCTGAAGTCCTACCAGCGCTGGTCCGGCTTCGAGGGCCCG
		1051 1100
2247	(1009)	ATCAACCTGGTGTACTCACAGCGCAACCGTTCGGCTGCTGTCCGTATCCC
13032	(1009)	ATCAACCTGGTGTACTCACAGCGCAACCGTTCGGCTGCTGTCCGTATCCC
CEFlnA1	(1009)	ATCAACCTGGTGTACTCACAGCGCAACCGTTCGGCGGCCGTCCGTATCCC
CEFlnA2	(1021)	GTGAGCGTGGCGTATTCGAGGAGAACCGTTCGGCGCGGATCCGATTCG
MtugInA2	(919)	ACGGCGCGCTCGTGGGGGGCCGCAACCGATCCGCCCTAGTCCGGGTGGC
MtugInA3	(922)	ATCTATGCATGCTGGGGTACCGAAACCGGGAAGCGGGGTCCGATTCGT
MtugInA4	(982)	ACGGCGCTGGCTTGGGGGTGGACAATCGCAGCTGCGCCCTCCGGGTG—
MtugInA1	(1012)	ATCAACCTGGTGTATAGCAGCGCAACCGTTCGGCATGCGTCCGCATCCC
Consensus	(1051)	ATCAACCTGGTGTATGAGCGCAACCGTCCGC GC GTGCG ATCCC
		1101 1150
2247	(1059)	AAT—CACCGGATCCAACCCGAAGGCAAGCGCATCGAATTCGGCGCTC
13032	(1059)	AAT—CACCGGATCCAACCCGAAGGCAAGCGCATCGAATTCGGCGCTC
CEFlnA1	(1059)	GAT—CACCGGTTCCAACCCGAAGGCAAGCGCATCGAGTTCGGCGCAC
CEFlnA2	(1071)	GGC—CAGCGGTCCAACCCGAAGGCAAGCGCATCGAGTTCGGCACCC
MtugInA2	(969)	GATGTACAGCCGCAACAAGACCTCGTCCGGCGGGTCCAAGTAAGCAGCC
MtugInA3	(972)	CAAGGCGGGCTGGCAGCGCGTACCGCGGGAACGTGAGGTGAAGCTCG
MtugInA4	(1030)	GTTGGCCACGGG—CAAAACAT—C—CGGGTCCAATCCCGCGTTC
MtugInA1	(1062)	GAT—CACCGGCAGCAACCCGAAGGCAAGCGGCTCGAGTTCGGAAGCC
Consensus	(1101)	GAT CACCGG CCAACCCGAAGGC AAGCGCATCGAGTTCGGCGCC
		1151 1200
2247	(1106)	CAGACCCATCAGGCAACCCATACCTGGGCTTCGCAGCGATGATGATGGCC
13032	(1106)	CAGACCCATCAGGCAACCCATACCTGGGCTTCGCAGCGATGATGATGGCC
CEFlnA1	(1106)	CGGACCCATCCGGCAACCCCTACCTGGGCTTCGCCGCCATGATGATGGCC
CEFlnA2	(1118)	CGGACCCCTCGGGTAACCCCTACCTGGGCTTCACCGCTCGATGATGGCG
MtugInA2	(1019)	CTGATTTCGGCGTGCAATCCCTATCTGACATTCGCCCTGCTGCTGGCGCG
MtugInA3	(1022)	TCGAGCCGTCCGGCAACCCCTATCTCGGTCGGCGCGGATCTTCGGAATG
MtugInA4	(1070)	CCGGCGGTGATGTCAACAGTAGCTGGCGGTGGCGGCTCTCATTCGTGGA
MtugInA1	(1109)	CCGACTCGTCCGGCAACCCGTATCTGGCGTTCGGCCATGCTGATGGCA
Consensus	(1151)	C GACCC TCGGGCAACCC TACCTGGCGTTCGC GCGATGATGATGGC
		1201 1250
2247	(1156)	GGCCTCGACGGCATCAAGAACCGCATCGAGCCACACGCTCCAGTGGACAA
13032	(1156)	GGCCTCGACGGCATCAAGAACCGCATCGAGCCACACGCTCCAGTGGACAA
CEFlnA1	(1156)	GGCCTGGACGGTGTGAAGAACCGCATCGAGCCGACGCAACCGGTGGACAA
CEFlnA2	(1168)	GGCCTGGACGGCATCCGCACCGCATCGAACCAGACGCCCTCTGGACAA
MtugInA2	(1069)	GGATTCCGGGGTGTAGAGAAGGTTAAGTGGTGGCCGGCAGGCCGAGGA
MtugInA3	(1072)	GCACTCGACGGCATGAAGACCAAGGCGCTGTTGCCGTCCGAAACGACCGT
MtugInA4	(1120)	GGGTGTACGGTATCGAGCGGGGCTTCAGCTGCCCGAGCCCTGTCTGGG
MtugInA1	(1159)	GGCCTGGACGGTATCAAGAACAAGATCGAGCCGACGCGCCGCTGACAA
Consensus	(1201)	GGCCTGGACGGTATCAAGAACCGCATCGAGCCGACGCGCC GTGGACAA
		1251 1300
2247	(1206)	GGACCTCTACGAACTGCCACGAGGGAAGCTGCATCCAT-----TCCAC
13032	(1206)	GGACCTCTACGAACTACCACGAGGGAAGCTGCATCCAT-----TCCAC
CEFlnA1	(1206)	GGACCTCTACGAGCTCCACCGGAGGAGGCCCGCTCCAT-----CCCGC
CEFlnA2	(1218)	GGACCTCTATGAGCTCCCGCCCAGGAGGGGTGCCAAGGT-----GGCCG

MtugInA2 (1119) CAACGTAATGGGACCTCACACCGAGGAACGCCGAGCGATGGGGTACCGAG  
 MtugInA3 (1122) AGACCCGACACAGCTGTCTGACGTGGATCGTACCGTGCCGGCATTCTGC  
 MtugInA4 (1170) CAACG-----CCT---ACC---AAGCGCCGATGT-----CGAAC  
 MtugInA1 (1209) GGATCTCTACGAGCTGCCCGGGAAGAGCGCGGAGTAT-----CCCGC  
 Consensus (1251) GGACCTCTACGAGCT CCACC GAGGAAGCTGCC C AT CCCAC  
 1301 1350  
 2247 (1250) AGGCACCAACCTCCCTGGAAGCATCCCTGAAGGCACTGCAGGAAGACACC  
 13032 (1250) AGGCACCAACCTCCCTGGAAGCATCCCTGAAGGCACTGCAGGAAGACACC  
 CEFgInA1 (1250) AGGCACCGACCTCCCTGGAAGCATCCCTGAAGGCCCTGCAGGAGGACTCC  
 CEFgInA2 (1262) AGGCCCCACCTCACTGGAACAGCGGCTGAAGGCCCTGGAGGAGGACAC  
 MtugInA2 (1169) AATTGCGTCCAGTTTGGATAGTGGCTCCGCGCATGGAGGC-----CTCC  
 MtugInA3 (1172) GACTTGTGCGGATCAGCCGATGCAATTGCTGTACTGGATAG-----TTCC  
 MtugInA4 (1199) GCTGCGGTTACGCTGGCCGACCGCGCGTGTCTGTTCCAGGA-----TTCT  
 MtugInA1 (1253) AGACTCCGACCCAGCTGTACAGATGTGATCGACCGTCTCGAGGCCGACAC  
 Consensus (1301) AGGC CCGACCTC CTGGAAGA GCCCTGAAGGC CTGGAGGA GACTCC  
 1351 1400  
 2247 (1300) GACTTCCTCACCAGTCTGACGTCCTCACCAGGAGATCTCATCGA-GGCGT  
 13032 (1300) GACTTCCTCACCAGTCTGACGTCCTCACCAGGAGATCTCATCGA-GGCGT  
 CEFgInA1 (1300) GACTTCCTCACCAGTCCGACGTGTCACCAGGAGCCTCATCGA-GGCCCT  
 CEFgInA2 (1312) GAGTTCCTCACCAGGGTGACGTGTCACCGATGATCTCATCGA-GGCCCT  
 MtugInA2 (1216) GAACCTGTCGCGGAG-----GCCCTGGGGGAGCAGTTTTTGA-CTTTT  
 MtugInA3 (1218) GAAACTGCTTCGGTG-----CATCCITGGCGATCCCGTGGTAGATGCCGT  
 MtugInA4 (1246) GCGCTGGTGGCGGAG-----GCCCTGGCGAGGATGTTGTCCG-CCACT  
 MtugInA1 (1303) GAATACCTCACCGAAGGAGGGGTGTTACAAAACGACCTGATCGA-GACGT  
 Consensus (1351) GA TTCCTCACCAG GACGTGTTACCGAGGATCTCATCGA GGCGT  
 1401 1450  
 2247 (1349) ACATCCAGTACAAGTAC-----GACAACGAGATCTCCCCAGTTGCGCTGCGC  
 13032 (1349) ACATCCAGTACAAGTAC-----GACAACGAGATCTCCCCAGTTGCGCTGCGC  
 CEFgInA1 (1349) ACATCCAGTACAAGTAC-----GACAACGAGATCACCCCGTTGCGCTGCGC  
 CEFgInA2 (1361) ATGTGGCTACAAGCAT-----GAACATGAGATCACCCCGTTGAGCGTCTGCGC  
 MtugInA2 (1259) TCTTGGCAACAAGCGCACGGAGTGGGCGAACTACCGCAGCCACGTACAG  
 MtugInA3 (1263) GGTCCGGGTACGCCAGT-TAGAGCATGACCGGTAC-----GGTGACCTCGAT  
 MtugInA4 (1289) ACCTGAACAAGCGCGCTGTGGAGCTGGCGCGCTTCAACCGCGCGGTCA-----  
 MtugInA1 (1352) GGATCAGTTTCAAGCGC-----GAAACGAGATCGAGCCGTTCAACATCCGG  
 Consensus (1401) ACATGCAGTACAAGCGC GA AACGAGATCTCCCC GT CGCCTGCGC  
 1451 1495  
 2247 (1396) CCAACCCCGCAGGAATTCGAATTGTACTTCGACTGC-----  
 13032 (1396) CCAACCCCGCAGGAATTCGAATTGTACTTCGACTGCTAA-----  
 CEFgInA1 (1396) CCAACCCCGCAGGAGTTCGAGCTGTACTTCGACTGCTAG-----  
 CEFgInA2 (1408) CCAACCGCTCTGGATTTCGAGCTGTACTTCGACTGCTAG-----  
 MtugInA2 (1309) CCATACGAGCTCCGCACCTACCTGTCGCTGTAG-----  
 MtugInA3 (1309) CCTGCGGAGCTGGCCGACAGTTCGGATGGCTTGGAGTGTGTAA  
 MtugInA4 (1337) CCGATTGGGAGAGGATACGTGGATTGACCGCTCTAG-----  
 MtugInA1 (1399) CCGCATCCCTACGAATTCGCGCTGTACTTCGAGCTTTAA-----  
 Consensus (1451) CC ACCCCGACAGGAATTCGAGCTGTACTTCGACTGCTA

2247 : B. flavum ATCC14067

13032 : C. glutamicum ATCC13032

CEF : C. efficiens YS314

Mtu : Mycobacterium tuberculosis H37RV